GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 2, 2004, 14:00:47 ; Search time 32049 Seconds
                                                  (without alignments)
                                                  11691.489 Million cell updates/sec

Title: US-10-038-854-37
Perfect score: 8645
Sequence: 1 tttggcctcgggccagaatt...............actgtatttaactaacttta 8645

Scoring table: IDENTITY_NUC
                       Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                 1:    gb_ba:*
                 2:    gb_htg:*
                 3:    gb_in:*
                 4:    gb_om:*
                 5:    gb_ov:*
                 6:    gb_pat:*
                 7:    gb_ph:*
                 8:    gb_pl:*
                 9:    gb_pr:*
                10:    gb_ro:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result | | Query | | | |
| No. | Score | %
Match | Length | DB | ID | Description |

11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

1	8645	100.0	8645	6	AX662355	AX662355 Sequence
2	8616.6	99.7	8675	6	AX662353	AX662353 Sequence
3	8000.6	92.5	8473	6	AX662357	AX662357 Sequence
4	7895.8	91.3	8487	6	AX662359	AX662359 Sequence
5	6789.2	78.5	8964	10	AB025412	AB025412 Mus muscu
6	5749.4	66.5	7816	10	AF195418	AF195418 Mus muscu
7	5305.8	61.4	5309	9	AB040888	AB040888 Homo sapi
8	4561.4	52.8	5804	10	AK122513	AK122513 Mus muscu
9	4273.8	49.4	8816	5	AB026979	AB026979 Danio rer
10	3714.8	43.0	8575	6	AX921803	AX921803 Sequence
11	3614	41.8	3614	6	AX876525	AX876525 Sequence
12	3614	41.8	3614	6	BD156175	BD156175 Primer fo
13	3614	41.8	3614	9	AK001336	AK001336 Homo sapi
14	3589.8	41.5	8438	6	AX675551	AX675551 Sequence
15	3566.6	41.3	8409	5	GGA279031	GGA279031 Gallus ga
16	3566.6	41.3	8409	6	AX250068	AX250068 Sequence
17	3545.6	41.0	8797	6	AX250063	AX250063 Sequence
18	3545.6	41.0	8797	6	AX250066	AX250066 Sequence
19	3545.6	41.0	8797	10	AB025411	AB025411 Mus muscu
20	3518.4	40.7	8689	6	AX250067	AX250067 Sequence
21	3518.4	40.7	8689	10	AF086607	AF086607 Rattus no
22	3502.2	40.5	8354	6	AX556500	AX556500 Sequence
23	3482.2	40.3	9826	6	AX250008	AX250008 Sequence
24	3453.8	40.0	9729	6	AX250013	AX250013 Sequence
25	3451.6	39.9	8585	10	AB025413	AB025413 Mus muscu
26	3439.2	39.8	8645	6	AX600210	AX600210 Sequence
27	3270	37.8	3270	6	AX877449	AX877449 Sequence
28	3270	37.8	3270	6	BD156663	BD156663 Primer fo
29	3270	37.8	3270	9	AK001748	AK001748 Homo sapi
30	3267.6	37.8	9722	10	AF059485	AF059485 Mus muscu
31	3235.6	37.4	3394	9	AK125869	AK125869 Homo sapi
32	3158	36.5	7781	9	AB032953	AB032953 Homo sapi
33	3066.4	35.5	9264	5	AB026980	AB026980 Danio rer
34	3012.6	34.8	8118	5	GGA238613	AJ238613 Gallus ga
35	2991.8	34.6	8373	10	AB025410	AB025410 Mus muscu
36	2970.8	34.4	7713	9	HSM808325	BX648178 Homo sapi
37	2854.8	33.0	8297	9	AF100772	AF100772 Homo sapi
38	2599	30.1	6560	6	AX250065	AX250065 Sequence
39	2155.4	24.9	2157	6	AX876360	AX876360 Sequence

40	2155.4	24.9	2157	6	BD156088
41	2155.4	24.9	2157	9	AK027473
42	1978.8	22.9	8993	9	HSM806812
43	1671.2	19.3	8624	9	AB037723
44	1658.8	19.2	5583	10	AK1224490
45	1614.8	18.7	184032	9	AC079226

BD156088 Primer fo
AK027473 Homo sapi
BX640737 Homo sapi
AB037723 Homo sapi
AK1224490 Mus muscu
AC079226 Homo sapi

Search completed: August 3, 2004, 06:21:49
Job time : 32211 secs

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OM nucleic - nucleic search, using sw model

Run on: August 2, 2004, 20:38:12 ; Search time 3396 Seconds
                                             (without alignments)
                                             12481.639 Million cell updates/sec

Title:
Perfect score: US-10-038-854-37
Sequence: 8645
                 1 tttggcctcgggccagaatt............actgtatttaactaacttta 8645

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 3222919 seqs, 2451570024 residues

Total number of hits satisfying chosen parameters: 6445838

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Database :   Published_Applications_NA:*
                 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
                 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
                 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
                 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	8645	100.0	8645	17	US-10-038-854-37	Sequence 37, Appl
2	8616.6	99.7	8675	17	US-10-038-854-35	Sequence 35, Appl
3	8000.6	92.5	8473	17	US-10-038-854-39	Sequence 39, Appl
4	7895.8	91.3	8487	17	US-10-038-854-41	Sequence 41, Appl
5	3714.8	43.0	8575	13	US-10-072-012-143	Sequence 143, App
6	3614	41.8	3614	13	US-10-342-887-1743	Sequence 1743, Ap
7	3614	41.8	3614	13	US-10-172-118-1743	Sequence 1743, Ap
8	3589.8	41.5	8438	13	US-10-042-865-1	Sequence 1, Appli
9	3566.6	41.3	8409	9	US-09-808-602-79	Sequence 79, Appl
10	3566.6	41.3	8409	10	US-09-800-198-67	Sequence 67, Appl
11	3545.6	41.0	8797	9	US-09-808-602-74	Sequence 74, Appl
12	3545.6	41.0	8797	9	US-09-808-602-77	Sequence 77, Appl
13	3545.6	41.0	8797	10	US-09-800-198-62	Sequence 62, Appl
14	3545.6	41.0	8797	10	US-09-800-198-65	Sequence 65, Appl
15	3518.4	40.7	8689	9	US-09-808-602-78	Sequence 78, Appl
16	3518.4	40.7	8689	10	US-09-800-198-66	Sequence 66, Appl
17	3502.2	40.5	8354	13	US-10-383-201-43	Sequence 43, Appl
18	3502.2	40.5	8354	13	US-10-029-020-13	Sequence 13, Appl
19	3482.2	40.3	9826	9	US-09-808-602-7	Sequence 7, Appli
20	3482.2	40.3	9826	10	US-09-800-198-7	Sequence 7, Appli
21	3466.4	40.1	9695	16	US-10-144-194A-81	Sequence 81, Appl

ALIGNMENTS

22	3453.8	40.0	9729	9	US-09-808-602-12	Sequence 12, Appl
23	3453.8	40.0	9729	10	US-09-800-198-12	Sequence 12, Appl
24	3264.8	37.8	9058	16	US-10-144-194A-79	Sequence 79, Appl
25	3249.6	37.6	8355	13	US-10-383-201-55	Sequence 55, Appl
26	2854.8	33.0	12880	16	US-10-295-027-927	Sequence 927, App
27	2599	30.1	6560	9	US-09-808-602-76	Sequence 76, Appl
28	2599	30.1	6560	10	US-09-800-198-64	Sequence 64, Appl
C 29	912.8	10.6	3217	15	US-10-198-846-13976	Sequence 13976, A
30	766.4	8.9	791	13	US-09-823-245A-85	Sequence 85, Appl
31	706	8.2	2496	9	US-09-808-602-75	Sequence 75, Appl
32	706	8.2	2496	10	US-09-800-198-63	Sequence 63, Appl
33	663.8	7.7	1399	13	US-10-383-201-49	Sequence 49, Appl
34	663.8	7.7	1399	13	US-10-383-201-59	Sequence 59, Appl
35	622	7.2	1392	13	US-10-383-201-45	Sequence 45, Appl
36	622	7.2	1392	13	US-10-383-201-53	Sequence 53, Appl
37	621.2	7.2	1476	13	US-10-383-201-41	Sequence 41, Appl
38	617.8	7.1	1371	13	US-10-383-201-51	Sequence 51, Appl
39	584.4	6.8	1755	10	US-09-998-966-17	Sequence 17, Appl
40	584.4	6.8	1755	15	US-10-004-415-17	Sequence 17, Appl
41	584.4	6.8	1755	16	US-10-384-974-17	Sequence 17, Appl
C 42	556.6	6.4	1973	9	US-09-864-761-4526	Sequence 4526, Ap
43	423	4.9	829	13	US-10-383-201-47	Sequence 47, Appl
44	423	4.9	829	13	US-10-383-201-61	Sequence 61, Appl
45	421.6	4.9	452	9	US-09-563-817-960	Sequence 960, App